

A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.9 bits)
 S2: 63 (29.0 bits)
 BLASTP 2.0.9 [May-07-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 47-14-1-C3-CL0_5C
 (351 letters)

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
 113,759 sequences; 24,820,038 total letters

Searching.....done

Sequences producing significant alignments:			Score (bits)	E Value
GSP:Y35918 Y35918 Extended human secreted protein sequence, SEQ...			735	0.0
STR:Q9ULS1 Q9ULS1 KIAA1149 PROTEIN (FRAGMENT). >GNP:AB032975 AB...			684	0.0
GSP:Y88438 Y88438 Modified human aspartyl protease 2 (Asp2) ami...			655	0.0
GNP:AF200193 AF200193_1 Homo sapiens memapsin 2 mRNA, partial c...			655	0.0
SP:P56817 Q9UJT5 BACE_HUMAN BETA-SECRETASE PRECURSOR (EC 3.4.23...			655	0.0
GSP:Y88439 Y88439 Modified human aspartyl protease 2 (Asp2) ami...			655	0.0
GSP:Y88437 Y88437 Human Asp2 amino acid sequence containing pro...			653	0.0
GSP:Y88425 Y88425 Human aspartyl protease 2 (a) (Asp2) amino ac...			653	0.0
GSP:Y88431 Y88431 T7-caspase-human-pro-Asp-2(a)-deltaTM amino a...			653	0.0
GSP:Y88432 Y88432 T7-caspase-human-pro-Asp-2(a)-deltaTM amino a...			653	0.0
GSP:Y88433 Y88433 Human-pro-Asp-2(a)-deltaTM amino acid sequence.			653	0.0
GSP:W59807 W59807 Amino acid sequence of human ASP2 (aspartic p...			653	0.0
GSP:W59808 W59808 Partial amino acid sequence of human ASP2 (as...			649	0.0
GSP:Y88426 Y88426 Human aspartyl protease 2 (b) (Asp2) amino ac...			592	e-169
GNP:AF200192 AF200192_1 Homo sapiens memapsin 1 mRNA, complete ...			362	e-100
SP:Q9Y5Z0 Q9UJT6 BAE2_HUMAN BETA SECRETASE 2 PRECURSOR (EC 3.4....			362	e-100
STR:CAB90554 CAB90554 Beta-site APP-cleaving enzyme 2, EC 3.4.2...			362	e-100
STR:AAF28927 AAF28927 HSPC104 (Fragment). >GNP:AF161367 AF16136...			300	3e-81
STR:AAF35836 AAF35836 Aspartyl protease. >GNP:AF188277 AF188277...			299	4e-81
STR:AAF35835 AAF35835 Aspartyl protease. >GNP:AF188276 AF188276...			262	5e-70
GSP:Y11427 Y11427 Human 5' EST secreted protein SEQ ID No 249.			118	2e-26
SP:P00790 PEPA_HUMAN PEPSIN A PRECURSOR (EC 3.4.23.1). >PIR:A00...			81	2e-15
PIR:A30142 S02664 S02542 PX0027 PX0025 PX0026 A22434 A30142 pep...			80	7e-15
GNP:M26032 M26032_1 Human pepsinogen A (15.0) gene, exon 9, clo...			80	7e-15
PIR:B30142 E22434 B30142 pepsin A (EC 3.4.23.1) 4 precursor - h...			79	1e-14
SP:P14091 CATE_HUMAN CATHEPSIN E PRECURSOR (EC 3.4.23.34). >PIR...			78	1e-14
SP:P07339 CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5). >GSP:...			76	1e-13
SP:P20142 PEPC_HUMAN GASTRISIN PRECURSOR (EC 3.4.23.3) (PEPSIN...			71	2e-12
GNP:M18667 M18667_1 Human pepsinogen C gene, exon 9, clone cosH...			71	2e-12
GSP:Y31744 Y31744 Human protease HPRM-3.			63	7e-10
STR:CAB82849 CAB82849 Cathepsin E, alternative precursor (EC 3....			63	7e-10
SP:P00797 RENI_HUMAN RENIN PRECURSOR, RENAL (EC 3.4.23.15) (ANG...			55	1e-07
GSP:P50135 P50135 Sequence of pre-pro-renin.			55	1e-07
GSP:W23244 W23244 Human renin.			55	1e-07
STR:Q15296 Q15296 KIDNEY MRNA FRAGMENT FOR RENIN (AA 105-401) (...			55	2e-07
GNP:M26901 M26901_1 Human renin gene, exon 9; precursor.			52	1e-06
GSP:W54877 W54877 Human napsin A protein.			38	0.030
GSP:W57042 W57042 Human aspartic protease SEQ ID NO:1.			38	0.030
GSP:Y44810 Y44810 Human Aspartic Protease-2 (NHAP-2).			38	0.030
STR:Q9UHB3 Q9UHB3 ASPARTYL PROTEASE 3 (FRAGMENT). >GNP:AF200344...			38	0.030
SP:O96009 NAP1_HUMAN NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A...			37	0.052
GSP:W37958 W37958 Amino acid sequence of human cathepsin polype...			37	0.052
GSP:Y06435 Y06435 Human protease HUPM-4. >GSP:Y44809 Y44809 Hum...			37	0.052
GSP:W57043 W57043 Human aspartic protease encoding cDNA SEQ ID ...			36	0.088
PIR:T08737 T08737 hypothetical protein DKFZp566O1646.1 - human ...			34	0.45
STR:AAF86877 AAF86877 DC8. >GNP:AF201941 AF201941_1 Homo sapien...			34	0.45
RTR:AAD53859 AAD53859 IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGIO...			32	1.7
SP:Q99712 Q99446 O00564 IRKF_HUMAN ATP-SENSITIVE INWARD RECTIFI...			29	8.7
GNP:D87291 D87291_1 Human mRNA for inward rectifier potassium c...			29	8.7
GNP:Y10745 Y10745_1 H.sapiens mRNA for inwardly rectifying potas...			29	8.7

>GSP:Y35918|Y35918|Extended human secreted protein sequence, SEQ ID

NO. 167.
Length = 351

Score = 735 bits (1878), Expect = 0.0
Identities = 351/351 (100%), Positives = 351/351 (100%)

Query: 1 MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI 60
MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI
Sbjct: 1 MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI 60

Query: 61 AAITESDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF 120
AAITESDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF
Sbjct: 61 AAITESDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF 120

Query: 121 PLNQSEVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKE 180
PLNQSEVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKE
Sbjct: 121 PLNQSEVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKE 180

Query: 181 YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI 240
YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI
Sbjct: 181 YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI 240

Query: 241 FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 300
FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
Sbjct: 241 FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 300

Query: 301 GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR
Sbjct: 301 GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351

>STR:Q9ULS1|Q9ULS1|KIAA1149 PROTEIN (FRAGMENT).
>GNP:AB032975|AB032975_1|Homo sapiens mRNA for KIAA1149
protein, partial cds; Start codon is not identified..
Length = 396

Score = 684 bits (1745), Expect = 0.0
Identities = 330/333 (99%), Positives = 330/333 (99%)

Query: 6 YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE 65
YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE
Sbjct: 1 YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE 60

Query: 66 SDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS 125
SDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS
Sbjct: 61 SDKFFINGSNWEIGLGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS 120

Query: 126 EVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 185
EVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK
Sbjct: 121 EVLASVGGSMIIGGIDHS LYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 180

Query: 186 SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS 245
SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS
Sbjct: 181 SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS 240

Query: 246 LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 305
LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV
Sbjct: 241 LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 300

Query: 306 FDRARKRIGFAVSACHVHDEFRTAAVEGPFCHL 338
FDRARKRIGFAVSACHVHDEFRTAAVEGPF L
Sbjct: 301 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTL 333

>GSP:Y88438|Y88438|Modified human aspartyl protease 2 (Asp2) amino
acid sequence.
Length = 453

Score = 655 bits (1672), Expect = 0.0
Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77
SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE
Sbjct: 118 SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMI 137
GILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMI

Sbjct: 178 GILGLAYAEIARPDDSLPEFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 238 GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257
PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 357

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417

Query: 318 SACHVHDEFRTAAVEGPFCHL 338
SACHVHDEFRTAAVEGPF L

Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GNP:AF200193|AF200193_1|Homo sapiens memapsin 2 mRNA, partial cds;
membrane-associated aspartic protease 2.
Length = 488

Score = 655 bits (1672), Expect = 0.0
Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77
SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 105 SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 164

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137
GILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII

Sbjct: 165 GILGLAYAEIARPDDSLPEFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 224

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 225 GGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 284

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257
PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF

Sbjct: 285 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 344

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 345 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 404

Query: 318 SACHVHDEFRTAAVEGPFCHL 338
SACHVHDEFRTAAVEGPF L

Sbjct: 405 SACHVHDEFRTAAVEGPFVTL 425

>SP:P56817 Q9UJT5|BACE_HUMAN|BETA-SECRETASE PRECURSOR (EC 3.4.23.-)
(BETA-SITE APP CLEAVING ENZYME) (BETA-SITE AMYLOID
PRECURSOR PROTEIN CLEAVING ENZYME) (ASPARTYLPROTEASE 2)
(ASP 2) (ASP2) (MEMBRANE-ASSOCIATED ASPARTIC PROTEASE
2) (MEMAPSIN-2). >PIR:A59090|A59090|aspartic proteinase
(EC 3.4.23.-) BACE precursor - human
>STR:AAF26367|AAF26367|Transmembrane aspartic proteinase
Asp 2. >GNP:AF190725|AF190725_1|Homo sapiens beta-site
APP cleaving enzyme (BACE) mRNA, complete cds.
>GNP:AF200343|AF200343_1|Homo sapiens chromosome 11
aspartyl protease 2 mRNA, complete cds.
>GNP:AF201468|AF201468_1|Homo sapiens APP beta-secretase
mRNA, complete cds; membrane type aspartyl protease.
>GNP:AF204943|AF204943_1|Homo sapiens transmembrane
aspartic proteinase Asp 2 (BACE1) mRNA, complete cds;
beta-site APP processing enzyme.
Length = 501

Score = 655 bits (1672), Expect = 0.0
Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77
SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 118 SSTYRDLRKGIVVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137

GILGLAYAEIARPD DS EPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII
 Sbjct: 178 GILGLAYAEIARPD DSLEPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII 237
 Query: 138 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL
 Sbjct: 238 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297
 Query: 198 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 257
 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF
 Sbjct: 298 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 357
 Query: 258 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 358 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88439|Y88439|Modified human aspartyl protease 2 (Asp2) amino
 acid sequence.
 Length = 459

Score = 655 bits (1672), Expect = 0.0
 Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 118 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE 177
 Query: 78 GILGLAYAEIARPD DSPEPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPD DS EPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII
 Sbjct: 178 GILGLAYAEIARPD DSLEPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII 237
 Query: 138 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL
 Sbjct: 238 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297
 Query: 198 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 257
 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF
 Sbjct: 298 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 357
 Query: 258 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 358 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88437|Y88437|Human Asp2 amino acid sequence containing
 proteolytic cleavage site.
 Length = 425

Score = 653 bits (1667), Expect = 0.0
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 90 SSTYRDLRKG VYVPYTQ GKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE 149
 Query: 78 GILGLAYAEIARPD DSPEPFFDSL VKQTHV PNL FSLQLCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPD DS EPFFDSL VKQTHV PNL FSL LCGAGFPLNQSEVLASVGGSMII
 Sbjct: 150 GILGLAYAEIARPD DSLEPFFDSL VKQTHV PNL FSLHLCGAGFPLNQSEVLASVGGSMII 209
 Query: 138 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL
 Sbjct: 210 GGIDHS LYTGSLWYTPIRREWY YEVII VRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 269
 Query: 198 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 257
 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF
 Sbjct: 270 PKKVFEAAVKS IKAASSTEKFDPD GFWLGEQLVCWQAGTTPWNI FFPVISLYLMGEVTNQSF 329
 Query: 258 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 330 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 389

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 390 SACHVHDEFRTAAVEGPFVTL 410

>GSP:Y88425|Y88425|Human aspartyl protease 2 (a) (Asp2) amino acid sequence.

Length = 501

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77

SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 118 SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137

GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII

Sbjct: 178 GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLHLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197

GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR

Sbjct: 238 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257

PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 357

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317

RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88431|Y88431|T7-caspase-human-pro-Asp-2(a)-deltaTM amino acid sequence.

Length = 446

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77

SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 111 SSTYRDLRKGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 170

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137

GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII

Sbjct: 171 GILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLLHLCGAGFPLNQSEVLASVGGSMII 230

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197

GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR

Sbjct: 231 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 290

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257

PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF

Sbjct: 291 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 350

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317

RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 351 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 410

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 411 SACHVHDEFRTAAVEGPFVTL 431

>GSP:Y88432|Y88432|T7-caspase-human-pro-Asp-2(a)-deltaTM amino acid sequence.

Length = 459

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 124 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 183

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII
 Sbjct: 184 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 243

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR
 Sbjct: 244 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 303

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257
 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF
 Sbjct: 304 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 363

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 364 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 423

Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 424 SACHVHDEFRTAAVEGPFVTL 444

>GSP:Y88433|Y88433|Human-pro-Asp-2(a)-deltaTM amino acid sequence.
 Length = 433

Score = 653 bits (1667), Expect = 0.0
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 98 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 157

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII
 Sbjct: 158 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 217

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR
 Sbjct: 218 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 277

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257
 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF
 Sbjct: 278 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 337

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 338 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 397

Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 398 SACHVHDEFRTAAVEGPFVTL 418

>GSP:W59807|W59807|Amino acid sequence of human ASP2 (aspartic
 protease 2).
 Length = 501

Score = 653 bits (1666), Expect = 0.0
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 118 SSTRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII
 Sbjct: 178 GILGLAYAEIARPDDSPPEFFDSLQKTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR
 Sbjct: 238 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF 357
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:W59808|W59808|Partial amino acid sequence of human ASP2
 (aspartic protease 2).
 Length = 790

Score = 649 bits (1655), Expect = 0.0
 Identities = 315/321 (98%), Positives = 315/321 (98%)

Query: 18 SSTYRDLRKGVPYPYTOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTYRDLRKGVPY TOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 61 SSTYRDLRKGVPYPYTOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 120
 Query: 78 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIARPDSD EPPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII
 Sbjct: 121 GILGLAYAEIARPDSDLEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 180
 Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL
 Sbjct: 181 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 240
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF 257
 PKKVFEAAVKSIIKAAS EKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF
 Sbjct: 241 PKKVFEAAVKSIIKAASPREKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF 300
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 301 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 360
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 361 SACHVHDEFRTAAVEGPFVTL 381

>GSP:Y88426|Y88426|Human aspartyl protease 2 (b) (Asp2) amino acid
 sequence.
 Length = 476

Score = 592 bits (1511), Expect = e-169
 Identities = 294/321 (91%), Positives = 294/321 (91%), Gaps = 25/321 (7%)

Query: 18 SSTYRDLRKGVPYPYTOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77
 SSTYRDLRKGVPYPYTOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE
 Sbjct: 118 SSTYRDLRKGVPYPYTOGKWEGLGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 177
 Query: 78 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 137
 GILGLAYAEIAR LCGAGFPLNQSEVLASVGGSMII
 Sbjct: 178 GILGLAYAEIAR-----LCGAGFPLNQSEVLASVGGSMII 212
 Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL
 Sbjct: 213 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 272
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF 257
 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF
 Sbjct: 273 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLSYLMGEVTNQSF 332
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV
 Sbjct: 333 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 392
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338
 SACHVHDEFRTAAVEGPF L
 Sbjct: 393 SACHVHDEFRTAAVEGPFVTL 413

>GNP:AF200192|AF200192_1|Homo sapiens memapsin 1 mRNA, complete cds;

membrane-associated aspartic protease 1.
Length = 518

Score = 362 bits (919), Expect = e-100
Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTVRANIAA 62
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA
Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+
Sbjct: 180 IFESENFFLPGIKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182
S + GGS+++GGI+ SLY G +WYTPI+ EWYY++ I+++EI GQ L +DC+EYN
Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 242
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFW G QL CW TPW+ FP
Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTITLPQQYL RVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302
IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF
Sbjct: 357 KISIIYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 415

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335
YV+FDRA+KR+GFA S C + + GPF
Sbjct: 416 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 448

>SP:Q9Y5Z0 Q9UJT6|BAE2_HUMAN|BETA SECRETASE 2 PRECURSOR (EC
3.4.23.-) (BETA-SITE APP-CLEAVING ENZYME 2) (ASPARTYL
PROTEASE 1) (ASP 1) (ASP1) (MEMBRANE-ASSOCIATED ASPARTIC
PROTEASE 1) (MEMAPSIN-1). >GSP:W61362|W61362|Aspartic
proteinase ASP1. >GSP:Y41714|Y41714|Human PRO852 protein
sequence. >GSP:Y22239|Y22239|Human CSP56, aspartyl-type
protease, protein sequence. >GSP:Y13799|Y13799|Human
aspartyl protease, CSP56. >GSP:Y88424|Y88424|Human
aspartyl protease 1 (Asp1) amino acid sequence.
>GNP:AF050171|AF050171_1|Homo sapiens aspartyl protease
mRNA, complete cds. >GNP:AF117892|AF117892_1|Homo
sapiens aspartic-like protease mRNA, complete cds.
>GNP:AF178532|AF178532_1|Homo sapiens aspartyl protease
(BACE2) mRNA, complete cds.
>GNP:AF200342|AF200342_1|Homo sapiens chromosome 21
aspartyl protease 1 mRNA, complete cds.
>GNP:AF204944|AF204944_1|Homo sapiens transmembrane
aspartic proteinase Asp 1 (BACE2) mRNA, complete cds;
beta-site APP processing enzyme.
>GNP:AF178532|AF178532_1|Homo sapiens aspartyl protease
(BACE2) mRNA, complete cds.
Length = 518

Score = 362 bits (919), Expect = e-100
Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTVRANIAA 62
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA
Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+
Sbjct: 180 IFESENFFLPGIKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182
S + GGS+++GGI+ SLY G +WYTPI+ EWYY++ I+++EI GQ L +DC+EYN
Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 242
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFW G QL CW TPW+ FP
Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTITLPQQYL RVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302
IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF
Sbjct: 357 KISIIYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 415

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335
 YV+FDRA+KR+GFA S C + + GPF
 Sbjct: 416 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 448

>STR:CAB90554|CAB90554|Beta-site APP-cleaving enzyme 2, EC 3.4.23
 (Fragment). >GNP:AL163285|AL163285_1|Homo sapiens
 chromosome 21 segment HS21C085; Accession No. AF050171.
 Length = 415

Score = 362 bits (919), Expect = e-100
 Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGNVTVRANIAA 62
 P Y+ +F + SSTYR V V YTOG W G +G DLV+IP G N + NIA
 Sbjct: 19 PHSYIDTYFD--TERSSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIAT 76

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSSPEPFDSLVKQTHVFNLFSLQLCGAGFPL 122
 I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+
 Sbjct: 77 IFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 136

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYN 182
 S + GGS+++GGI+ SLY G +WYTPI+ EWYY++ I+++EI GQ L +DC+EYN
 Sbjct: 137 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKBEWYQIEILKLEIGGQSLNLDCKEYN 193

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242
 DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFV G QL CW TPW+ FP
 Sbjct: 194 ADKAIVDSGTTLLRPLQKVFDVAVVEAVARSLIPEFSDGFWTGSQACWTNSETPWSYFP 253

Query: 243 VISLYLMGEVTNQSFRTITLPQQYLRPVEDVATSDQDDCYKFAISQSSTGTVMGAVIMEGF 302
 IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF
 Sbjct: 254 KISYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 312

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335
 YV+FDRA+KR+GFA S C + + GPF
 Sbjct: 313 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 345

>STR:AAF28927|AAF28927|HSPC104 (Fragment).
 >GNP:AF161367|AF161367_1|Homo sapiens HSPC104 mRNA,
 partial cds.
 Length = 213

Score = 300 bits (759), Expect = 3e-81
 Identities = 154/217 (70%), Positives = 164/217 (74%), Gaps = 7/217 (3%)

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 197
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR
 Sbjct: 1 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 60

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257
 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF
 Sbjct: 61 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 120

Query: 258 RITILPQQYLRPVE---DVATSDQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
 RITILPQQYLRP + T+ C+ I G+ ++ + + +
 Sbjct: 121 RITILPQQYLRPWKMWRPRTTTVTVCHLTVIHGHCYGCYHGGLPLSLIGPENELACLS 180

Query: 315 FAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351
 R A+ CHLGHGRLWLQHSTDR
 Sbjct: 181 ALAMCTMSSGRQRWKAL----CHLGHGRLWLQHSTDR 213

>STR:AAF35836|AAF35836|Aspartyl protease.
 >GNP:AF188277|AF188277_1|Homo sapiens aspartyl protease
 (BACE2) mRNA, complete cds, alternatively spliced;
 alternatively spliced; lacks exon 8.
 >GNP:AF188277|AF188277_1|Homo sapiens aspartyl protease
 (BACE2) mRNA, complete cds, alternatively spliced;
 alternatively spliced; lacks exon 8.
 Length = 396

Score = 299 bits (758), Expect = 4e-81
 Identities = 143/263 (54%), Positives = 186/263 (70%), Gaps = 5/263 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGNVTVRANIAA 62
 P Y+ +F + SSTYR V V YTOG W G +G DLV+IP G N + NIA

Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+

Sbjct: 180 IFESENFFLPGLKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182
S + GGS+++GGI+ SLY G +WYTPI+ EWYY++ I+++EI GQ L +DC+EYN

Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFV G QL CW TPW+ FP

Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTILPQQ 265
IS+YL E +++SFRITILPQ+

Sbjct: 357 KISYLRDENSRSFRITILPQK 379

>STR:AAF35835|AAF35835|Aspartyl protease.

>GNP:AF188276|AF188276_1|Homo sapiens aspartyl protease
(BACE2) mRNA, complete cds, alternatively spliced;
alternatively spliced; lacks exon 7.

>GNP:AF188276|AF188276_1|Homo sapiens aspartyl protease
(BACE2) mRNA, complete cds, alternatively spliced;
alternatively spliced; lacks exon 7.

Length = 468

Score = 262 bits (663), Expect = 5e-70

Identities = 143/333 (42%), Positives = 190/333 (56%), Gaps = 56/333 (16%)

Query: 3 PFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAA 62
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA

Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+

Sbjct: 180 IFESENFFLPGLKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182
S + GGS+++GGI+ SLY G +WYTPI+ EWYY++ I+++EI GQ L +DC+EYN

Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242
DK+IVDSGTT LRLP+KVF+A V+++ AS P G C++ G +P

Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLLYIQP-MMGAGLNYECYRFGISP----- 350

Query: 243 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302
S+ V+GA +MEGF

Sbjct: 351 -----STNALVIGATVMEGF 365

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335
YV+FDRA+KR+GFA S C + + GPF

Sbjct: 366 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 398

>GSP:Y11427|Y11427|Human 5' EST secreted protein SEQ ID No 249.
Length = 53

Score = 118 bits (292), Expect = 2e-26

Identities = 52/52 (100%), Positives = 52/52 (100%)

Query: 1 MVFFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP 52
MVFFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP

Sbjct: 1 MVFFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP 52

>SP:P00790|PEPA_HUMAN|PEPSIN A PRECURSOR (EC 3.4.23.1). >PIR:A00980
PX0023 S02663 F22434 I54252 PX0024|PEHU|pepsin A (EC
3.4.23.1) 3 precursor - human >GNP:J00287|J00287_1|Human
pepsinogen gene, exon 9; pepsinogen.
Length = 388

Score = 81.1 bits (197), Expect = 2e-15

Identities = 82/302 (27%), Positives = 137/302 (45%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76

SSTY+ + V + Y G G LG D V + ++ I ++E++ F+ + +
 Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77 EGILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSM 135
 +GILGLAY I+ P FD++ Q V +LFS+ L +QS G +
 Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLFVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHSPLYTGLSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
 I GGID S YTGSL + P+ E Y+++ + + +NG+ + C E ++IVD+GT+ L
 Sbjct: 228 IFGGIDSSYYTGLSNWVPVTVEGYWQITVDSITMNGEIAI--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
 P I A+ +++ G+ +V C + P +F T
 Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324

Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
 + + P Y+ E S ++S ++G V + ++ VFDRA ++G
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNLP-TEGELWILGDVFIRQYFTVFDRAANNQVG 383

Query: 315 FA 316
 A
 Sbjct: 384 LA 385

>PIR:A30142 S02664 S02542 PX0027 PX0025 PX0026 A22434|A30142|pepsin
 A (EC 3.4.23.1) 5 precursor - human
 Length = 388

Score = 79.6 bits (193), Expect = 7e-15
 Identities = 81/302 (26%), Positives = 137/302 (44%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76
 SSTY+ + V + Y G G LG D V + ++ I ++E++ F+ + +
 Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77 EGILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSM 135
 +GILGLAY I+ P FD++ Q V +LFS+ L +QS G +
 Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLFVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHSPLYTGLSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
 I GGID S YTGSL + P+ E Y+++ + + +NG+ + C E ++IVD+GT+ L
 Sbjct: 228 IFGGIDSSYYTGLSNWVPVTVEGYWQITVDSITMNGEIAI--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
 P I A+ +++ G+ +V C + P +F T
 Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324

Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
 + + P Y+ E S ++S ++G V + ++ VF+RA ++G
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNLP-TEGELWILGDVFIRQYFTVFERANNQVG 383

Query: 315 FA 316
 A
 Sbjct: 384 LA 385

>GNP:M26032|M26032_1|Human pepsinogen A (15.0) gene, exon 9, clone
 cgHGP2; precursor.
 Length = 388

Score = 79.6 bits (193), Expect = 7e-15
 Identities = 81/302 (26%), Positives = 137/302 (44%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76
 SSTY+ + V + Y G G LG D V + ++ I ++E++ F+ + +
 Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77 EGILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSM 135
 +GILGLAY I+ P FD++ Q V +LFS+ L +QS G +
 Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLFVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHSPLYTGLSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
 I GGID S YTGSL + P+ E Y+++ + + +NG+ + C E ++IVD+GT+ L
 Sbjct: 228 IFGGIDSSYYTGLSNWVPVTVEGYWQITVDSITMNGEIAI--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
 P I A+ +++ G+ +V C + P +F T

Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324
 Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
 + + P Y+ E S ++S ++G V + ++ VF+RA ++G
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNLP-TESGELWILGDVFIRQYFTVFERANNQVG 383
 Query: 315 FA 316
 A
 Sbjct: 384 LA 385

>PIR:B30142 E22434|B30142|pepsin A (EC 3.4.23.1) 4 precursor - human
 Length = 388

Score = 78.8 bits (191), Expect = 1e-14
 Identities = 79/302 (26%), Positives = 134/302 (44%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76
 SSTY+ + V + Y G G LG D V + ++ I ++E++ F+ + +
 Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179
 Query: 77 EGILGLAYAEIARPDDSPPEFFDSLVLKQTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSM 135
 +GILGLAY I+ P FD++ Q V +LFS+ L G +
 Sbjct: 180 DGILGLAYPSIS---SSGATPVFDNIWNQGLVSQLDFSVYLSADD-----KSGSVV 227
 Query: 136 IIGGIDHSPLYTGLSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
 I GGID S YTGSL + P+ E Y+++ + +NG+ + C E ++IVD+GT+ L
 Sbjct: 228 IFGGIDSSYYTGSNLNWPVTVVEGYWQITVDSITMNETIA--CAE--GCQAIVDTGTSLL 283
 Query: 196 RLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
 P I A+ +++ G+ +V C + P +F T
 Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324
 Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
 + + P Y+ E S ++S ++G V + ++ VF+RA ++G
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNVP-TESGELWILGDVFIRQYFTVFERANNQVG 383
 Query: 315 FA 316
 A
 Sbjct: 384 LA 385

>SP:P14091|CATE_HUMAN|CATHEPSIN E PRECURSOR (EC 3.4.23.34).
 >PIR:A42038 A34401 S35663 S34467 A34643
 B34643|A34401|cathepsin E (EC 3.4.23.34) precursor -
 human >STR:CAB82850|CAB82850|Procathepsin E precursor
 (EC 3.4.23.34). >GNP:AJ250717|AJ250717_1|Homo sapiens
 mRNA for procathepsin E (CatE gene).
 >GNP:J05036|J05036_1|Human cathepsin E mRNA, complete
 cds; cathepsin E precursor. >GNP:M84424|M84424_1|Human
 cathepsin E (CTSE) gene, exon 9 and complete cds.
 Length = 396

Score = 78.4 bits (190), Expect = 1e-14
 Identities = 83/325 (25%), Positives = 137/325 (41%), Gaps = 46/325 (14%)

Query: 2 VPFIYL----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTV 56
 VP +Y + H SSTY + + Y G G +G D VS+ G V
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIYGTGSLSGIIGADQVSV-EGLTVVG 162
 Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSLVLKQTHVPNLFSLQLC 116
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ----NLVDLPMF 215
 Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSPLYTGLSLWYTPIRREWYVEIIVRVEINGQDLKM 176
 N G +I GG DHS ++GSL + P+ ++ Y+++ + +++ G M
 Sbjct: 216 SVYMSSNPE--GGAGSELIFGGYDHSFSGSLNWPVTKQAYWQIALDNIQVGG--TVM 270
 Query: 177 DCKEYNYDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTT 236
 C E ++IVD+GT+ + P + +I AA DG + E
 Sbjct: 271 FCSE--GCQAIVDTGTSITGSPDKIKQLQNAIGAAP-----VDGEYAVE-----CA 315
 Query: 237 PWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT- 292
 N+ P ++ + G T+ P Y + D C ++ G
 Sbjct: 316 NLNVMPDVTFTING-----VPYTLSPYAY--TLLDFVDGMQFCSSGFQGLDIHPAGPL 367
 Query: 293 -VMGAVIMEGFYVVFDRARKRIGFA 316

++G V + FY VFDR R+G A
 Sbjct: 368 WILGDVFIRQFYSVFDRGNRVGLA 392

>SP:P07339|CATD_HUMAN|CATHEPSIN D PRECURSOR (EC 3.4.23.5).
 >GSP:R74207|R74207|Human death associated protein DAP-7,
 also called cathepsin D. >GSP:W71369|W71369|Death
 associated protein (DAP)-7 (cathepsin D).
 >GSP:Y06478|Y06478|Human tumour-associated protein
 PRO292. >PIR:A25771 S30749 PC2066 I59236
 I57716|KHHUD|cathepsin D (EC 3.4.23.5) precursor
 [validated] - human >GNP:X05344|X05344_1|Human mRNA for
 cathepsin D from oestrogen responsive breast cancer
 cells; precursor polypeptide (AA -20 to 392).
 >GNP:M63138|M63138_1|Human cathepsin D (catD) gene,
 exons 7, 8, and 9. >GNP:M11233|M11233_1|Human cathepsin
 D mRNA, complete cds; preprocathepsin D.
 Length = 412

Score = 75.7 bits (183), Expect = 1e-13
 Identities = 91/327 (27%), Positives = 138/327 (41%), Gaps = 53/327 (16%)

Query: 10 HFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHP-----GPNVTVRANI 60
 H S SSTY + Y G G L D VS+P G R
 Sbjct: 120 HHKYNDSKSSSTYVKNGTSTFDIHYGSGSLSGYLSQDTSVPCQSASSASALGGVKVERQVF 179
 Query: 61 AAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSL VKQTHVP-NLFSLQLCGAG 119
 T+ + ++GILG+AY I+ ++ P FD+L++Q V N+FS L
 Sbjct: 180 GEATKQPGITFIAAKFDGILGMAYPRISV--NNVLPVFDNLMQQKLVDQNIFS FYL---- 233
 Query: 120 FPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEI-NGQDLKMD C 178
 + A GG +++GG D Y GSL Y + R+ Y++V + +VE+ +G L C
 Sbjct: 234 ----SRDPDAQPGGELMLGGTDSKYKGSLSYLNVTRKAYWQVHLDQVEVASGLTL---C 286
 Query: 179 KEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTP 237
 KE ++IVD+GT+ + P K+I A + GE ++ C + T
 Sbjct: 287 KE--GCEAIVDTGTSLMVGVPVDEVRELQKAIGAVPLIQ-----GEYMIPCEKVST-- 334
 Query: 238 WNIFFVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQ-----SSTGT 292
 P I+L L G+ S P+ Y V + C + S
 Sbjct: 335 ---LPAILTKLGKGYKLS-----PEDYTLKVSQAGKTL--CLSGFMGMDIPPPSGPLW 383
 Query: 293 VMGAVIMEGFYVVFDRARKRIGFAVSA 319
 ++G V + +Y VFDR R+GFA +A
 Sbjct: 384 ILGDVFIGRYYTVFDRDNNRVGFAEAA 410

>SP:P20142|PEPC_HUMAN|GASTRISIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN
 C). >PIR:A29937 A31811 PX0028 I54213 A91125
 A23458|A29937|gastricsin (EC 3.4.23.3) precursor - human
 >GNP:U75272|U75272_1|Human gastricsin mRNA, complete
 cds; pepsinogen C; partial peptide sequencing.
 >GNP:M23077|M23077_1|Human pepsinogen gene, exon 9,
 clone PCG401; precursor. >GNP:J04443|J04443_1|Homo
 sapiens pepsinogen C (PGC) mRNA, complete cds;
 precursor.
 Length = 388

Score = 71.4 bits (172), Expect = 2e-12
 Identities = 78/329 (23%), Positives = 142/329 (42%), Gaps = 50/329 (15%)

Query: 2 VPFIYLQA-----HFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGPNVTV 56
 VP +Y Q+ H SSTY + Y G G G D +++ ++ V
 Sbjct: 99 VPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYSGSLTGFFGYDTLTVQ---SIQV 155
 Query: 57 RANIAAITESDKFFINGSNW-----EGILGLAYAEIARPDSPPEFFDSL VKQTHVPN-L 110
 ++E++ G+N+ +GI+GLAY ++ D +V++ + + +
 Sbjct: 156 PNQEFGLSENEP----GTNFVYAQFDGIMGLAYPALSV--DEATTAMQGMVQEGALTSPV 209
 Query: 111 FSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEIN 170
 FS+ L S S GG+++ GG+D SLYTG +++ P+ +E Y+++ I I
 Sbjct: 210 FSVYL-----SNQQGSSGGAUVFGGVDSLYTGQIYWAPVTQELYWQIGIEEFLIG 260
 Query: 171 GQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVC 230
 GQ C E ++IVD+GT+ L +P++ A +++ A G+ LV
 Sbjct: 261 GQASGW-CSE--GCQAIVDTGTSLLTVPQQYMSALLQATGAQEDE-----YGQFLV- 308

Query: 231 WQAGTTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSST 290
 N + +L + + N + P Y+ T + +
 Sbjct: 309 -----NCNSIQNLPSLTFTIIN-GVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQP 359

Query: 291 GTVMGAVIMEGFYVVFDRARKRIGFAVSA 319
 ++G V + +Y V+D R+GFA +A
 Sbjct: 360 LWILGDVFLRSYYSVYDLGNNRVGFATAA 388

>GNP:M18667|M18667_1|Human pepsinogen C gene, exon 9, clone
 cosHGPC44-1; prepropepsinogen C.
 Length = 385

Score = 71.4 bits (172), Expect = 2e-12
 Identities = 78/329 (23%), Positives = 142/329 (42%), Gaps = 50/329 (15%)

Query: 2 VPFIYLQA-----HFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56
 VP +Y Q+ H SSTY + + Y G G G D +++ ++ V
 Sbjct: 96 VPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYSGSLTGFFGYDTLTVQ---SIQV 152

Query: 57 RANIAAITESDKFFINGSNW-----EGILGLAYAEIARPDSPPEFFDSLQKTHVPN-L 110
 ++E++ G+N+ +GI+GLAY ++ D +V++ + + +
 Sbjct: 153 PNQEFGLSENEP---GTNFVYAQFDGIMGLAYPALSV--DEATTAMQGMVQEGALTSPV 206

Query: 111 FSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEVIVRVEIN 170
 FS+ L S S GG+++ GG+D SLYTG +++ P+ +E Y+++ I I
 Sbjct: 207 FSVYL-----SNQQGSSGGAUVFGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIG 257

Query: 171 GQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVC 230
 GQ C E ++IVD+GT+ L +P++ A +++ A G+ LV
 Sbjct: 258 GQASGW-CSE--GCQAIVDTGTSLLTVPQQYMSALLQATGAQEDE-----YGQFLV- 305

Query: 231 WQAGTTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSST 290
 N + +L + + N + P Y+ T + +
 Sbjct: 306 -----NCNSIQNLPSLTFTIIN-GVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQP 356

Query: 291 GTVMGAVIMEGFYVVFDRARKRIGFAVSA 319
 ++G V + +Y V+D R+GFA +A
 Sbjct: 357 LWILGDVFLRSYYSVYDLGNNRVGFATAA 385

>GSP:Y31744|Y31744|Human protease HPRM-3.
 Length = 349

Score = 62.8 bits (150), Expect = 7e-10
 Identities = 47/168 (27%), Positives = 78/168 (45%), Gaps = 16/168 (9%)

Query: 2 VPFIYL-----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56
 VP +Y + H SSTY + + Y G G +G D VS+ G V
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIYGTGSLSGIIGADQVSV-EGLTVVG 162

Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLC 116
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ---NLVDLPMF 215

Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEV 164
 N G +I GG DHS ++GSL + P+ ++ Y+++ +
 Sbjct: 216 SVYMSSNPE---GGAGSELIFGGYDHSFSGSLNWVPVTKQAYWQIAL 260

>STR:CAB82849|CAB82849|Cathepsin E, alternative precursor (EC
 3.4.23.34). >GNP:AJ250716|AJ250716_1|Homo sapiens mRNA
 for cathepsin E (CatE gene), alternative splicing,
 isolated from adenocarcinoma cell lines.
 Length = 363

Score = 62.8 bits (150), Expect = 7e-10
 Identities = 47/168 (27%), Positives = 78/168 (45%), Gaps = 16/168 (9%)

Query: 2 VPFIYL-----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56
 VP +Y + H SSTY + + Y G G +G D VS+ G V
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIYGTGSLSGIIGADQVSV-EGLTVVG 162

Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLC 116
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ---NLVDLPMF 215

Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVII 164
 N G +I GG DHS ++GSL + P+ ++ Y+++ +
 Sbjct: 216 SVYMSSNPE---GGAGSELIFGGYDHSFSGSLNWVPVTKQAYWQIAL 260

>SP:P00797|RENI_HUMAN|RENIN PRECURSOR, RENAL (EC 3.4.23.15)
 (ANGIOTENSINOGENASE). >PIR:A21454 A21190 A21673 A00990
 A26531 I52884 I55306 I53999 A35688 A36504 A27367
 A39906|REHUK|renin (EC 3.4.23.15) precursor - human
 >GNP:L00073|L00073_1|Human renin gene, exon 10;
 precursor. >GNP:M10152|M10152_1|Human renin gene, exon
 10.
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07
 Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

Query: 18 SSTYRDLRKGYYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+Y+ + + Y+ G G L D++++ +TV +TE + ++
 Sbjct: 135 SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78 GILGLAYAEIARDDSPPEFFDSLQKQTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
 G++G+ + E A P FD+++ Q + ++FS + SE S+GG ++
 Sbjct: 192 GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 243

Query: 137 IGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
 +GG D Y G+ Y + + +++ + V + L + + ++VD+G + +
 Sbjct: 244 LGGSDPQHYEGNFHYINLIKTVGWQIQMKGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256
 + SS EK + ++L + P IS +L G+
 Sbjct: 300 -----GSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
 T+ Y+ ++ +S+ C + I + T +GA + FY FDR
 Sbjct: 342 -EYTLTSADYV--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312 RIGFAVS 318
 RIGFA++
 Sbjct: 399 RIGFALA 405

>GSP:P50135|P50135|Sequence of pre-pro-renin.
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07
 Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

Query: 18 SSTYRDLRKGYYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+Y+ + + Y+ G G L D++++ +TV +TE + ++
 Sbjct: 135 SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78 GILGLAYAEIARDDSPPEFFDSLQKQTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
 G++G+ + E A P FD+++ Q + ++FS + SE S+GG ++
 Sbjct: 192 GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 243

Query: 137 IGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
 +GG D Y G+ Y + + +++ + V + L + + ++VD+G + +
 Sbjct: 244 LGGSDPQHYEGNFHYINLIKTVGWQIQMKGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256
 + SS EK + ++L + P IS +L G+
 Sbjct: 300 -----GSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
 T+ Y+ ++ +S+ C + I + T +GA + FY FDR
 Sbjct: 342 -EYTLTSADYV--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312 RIGFAVS 318
 RIGFA++
 Sbjct: 399 RIGFALA 405

>GSP:W23244|W23244|Human renin.
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07

Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 135  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      + SE S+GG ++
Sbjct: 192  GVVGMGFIEQAI--GRVTPIFDNIISQGVLEKEDVFSF-----YYNRDSSENSQSLGGQIV 243

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 244  LGGSDPQHIEGNFHYINLIKTGVWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197  LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ 256
          + SS EK +   ++L +   P IS +L G+
Sbjct: 300  -----GSTSSIEKLMEALGAKRFLDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257  FRITILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
          T+   Y+   ++ +S+ C   + I + T +GA + FY FDR
Sbjct: 342  -EYTLTSADYV--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312  RIGFAVS 318
          RIGFA++
Sbjct: 399  RIGFALA 405

```

>STR:Q15296|Q15296|KIDNEY MRNA FRAGMENT FOR RENIN (AA 105-401)
 (FRAGMENT). >GNP:X00063|X00063_1|Human kidney mRNA
 fragment for renin (aa 105-401); renin (aa 105 to 401).
 Length = 300

Score = 55.0 bits (130), Expect = 2e-07

Identities = 70/307 (22%), Positives = 133/307 (42%), Gaps = 41/307 (13%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 28  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 84

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      + SE S+GG ++
Sbjct: 85  GVVGMGFIEQAI--GRVTPIFDNIISQGVLEKEDVFSF-----YYNRDSSENSQSLGGQIV 136

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 137  LGGSDPQHIEGNFHYINLIKTGVWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 192

Query: 197  LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ 256
          E   K ++A + EK      L + +V   G T   P IS +L G+
Sbjct: 193  GSTSSIE---KLMEALGAKEKR-----LFDYVVKCNEGPT----LPDISFHLGGK----- 235

Query: 257  FRITILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
          T+   Y+   ++ +S+ C   + I + T +GA + FY FDR
Sbjct: 236  -EYTLTSADYI--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 292

Query: 312  RIGFAVS 318
          RIGFA++
Sbjct: 293  RIGFALA 299

```

>GNP:M26901|M26901_1|Human renin gene, exon 9; precursor.
 Length = 403

Score = 52.3 bits (123), Expect = 1e-06

Identities = 67/307 (21%), Positives = 132/307 (42%), Gaps = 45/307 (14%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 135  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAQFD 191

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      F N++ S+GG ++
Sbjct: 192  GVVGMGFIEQAI--GRVTPIFDNIISQGVLEKEDVFS-----FYYNRNS--QSLGGQIV 240

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 241  LGGSDPQHIEGNFHYINLIKTGVWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 296

```


Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256
 E ++++ A L + +V G T P IS +L G+
 Sbjct: 297 GSTSCIEKLMEALGAKKR-----LFDYVVVKNEGPT----LPDISFHLGGK----- 338

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
 T+ Y+ ++ +S+ C + I + T +GA + FY FDR
 Sbjct: 339 -EYTLTSADYV--FQESYSSKKLCTLAIHAMDIPPPTGPTWALGATFIRKFYTEFDRRNN 395

Query: 312 RIGFAVS 318
 RIGFA++
 Sbjct: 396 RIGFALA 402

>GSP:W54877|W54877|Human napsin A protein.
 Length = 451

Score = 37.5 bits (85), Expect = 0.030
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+++ + Y G+ +G L D ++I +V A S F + S +
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172
 +GG D + Y L + P+ Y+++ + RV++ +
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>GSP:W57042|W57042|Human aspartic protease SEQ ID NO:1.
 Length = 438

Score = 37.5 bits (85), Expect = 0.030
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+++ + Y G+ +G L D ++I +V A S F + S +
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172
 +GG D + Y L + P+ Y+++ + RV++ +
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>GSP:Y44810|Y44810|Human Aspartic Protease-2 (NHAP-2).
 Length = 433

Score = 37.5 bits (85), Expect = 0.030
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+++ + Y G+ +G L D ++I +V A S F + S +
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172
 +GG D + Y L + P+ Y+++ + RV++ +
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>STR:Q9UHB3|Q9UHB3|ASPARTYL PROTEASE 3 (FRAGMENT).
 >GNP:AF200344|AF200344_1|Homo sapiens aspartyl protease
 3 mRNA, partial cds.
 Length = 450

Score = 37.5 bits (85), Expect = 0.030

Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKG VYVPYTQ GKWEGELGTDLV SIPHGP NVTVRANIAA ITESDKFFINGSNWE 77
 SS+++ + Y G+ +G L D ++I +V A S F + S +
 Sbjct: 127 SSSFKPSG TKFAI QYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIAR PDDSP EPPFFDSL VKQTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172
 +GG D + Y L + P+ Y+++ + RV++ +
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>SP:096009|NAP1_HUMAN|NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A)
 (NAPA) (TA01/TA02) (ASPARTYL PROTEASE 4) (ASP 4) (ASP4).
 >GSP:W54878|W54878|Human napsin B protein.
 >GNP:AF090386|AF090386_1|Homo sapiens napsin A mRNA,
 complete cds; aspartic proteinase.
 >GNP:AF098484|AF098484_1|Homo sapiens napsin 1
 precursor, mRNA, complete cds.
 >GNP:AF200345|AF200345_1|Homo sapiens aspartyl protease
 4 mRNA, complete cds.
 Length = 420

Score = 36.7 bits (83), Expect = 0.052
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQ GKWEGELGTDLV SIPHGP NVTVRANIAA ITESDKFFINGSNWE GILGLAYAEIAR 89
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSP EPPFFDSL VKQTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148
 + P D LV+Q + +FS F LN+ GG +++GG D + Y
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKKVFEA 204
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAKGC---AAILDTGTSLITGPTTEEIRA 298

>GSP:W37958|W37958|Amino acid sequence of human cathepsin
 polypeptide-2.
 Length = 395

Score = 36.7 bits (83), Expect = 0.052
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQ GKWEGELGTDLV SIPHGP NVTVRANIAA ITESDKFFINGSNWE GILGLAYAEIAR 89
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSP EPPFFDSL VKQTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148
 + P D LV+Q + +FS F LN+ GG +++GG D + Y
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKKVFEA 204
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAKGC---AAILDTGTSLITGPTTEEIRA 298

>GSP:Y06435|Y06435|Human protease HUPM-4. >GSP:Y44809|Y44809|Human
 Aspartic Protease-1 (NHAP-1). >GSP:Y44457|Y44457|Human
 lung specific gene protein Lngl05.
 Length = 420

Score = 36.7 bits (83), Expect = 0.052
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQ GKWEGELGTDLV SIPHGP NVTVRANIAA ITESDKFFINGSNWE GILGLAYAEIAR 89
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSP EPPFFDSL VKQTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148
 + P D LV+Q + +FS F LN+ GG +++GG D + Y
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAGKC---AAILDTGTSITGPTEEIRA 298

>GSP:W57043|W57043|Human aspartic protease encoding cDNA SEQ ID
 NO:15.
 Length = 449

Score = 36.0 bits (81), Expect = 0.088
 Identities = 44/178 (24%), Positives = 80/178 (44%), Gaps = 21/178 (11%)

Query: 18 SSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
 SS+++ + Y G+ +G L D ++I +V A S F + S +
 Sbjct: 146 SSSFKPSGKTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 203

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136
 GILGL + ++ + P D LV+Q + +FS F N+ + + GG ++
 Sbjct: 204 GILGLGFILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRPDPEVVN-GGELV 253

Query: 137 IGGIDHSLYTGSWYTPIRREWYVEIIVRVEI--NGQDLKMDCKEYNYDKSIVDSGT 192
 +GG D + Y L + P+ Y+++ + RV++ L C +I+D+GT
 Sbjct: 254 LGGSDPAHYIPLNFPVTVPAYWQIHMERVKVGPRA DSLCQGC-----AAILDTGT 305

>PIR:T08737|T08737|hypothetical protein DKFZp566O1646.1 - human
 (fragment) >STR:Q9Y415|Q9Y415|HYPOTHETICAL 25.3 KDA
 PROTEIN (FRAGMENT). >GNP:AL050084|AL050084_1|Homo
 sapiens mRNA; cDNA DKFZp566O1646 (from clone
 DKFZp566O1646); partial cds; weak similarity to
 S.cerevisiae Zip1p.
 Length = 218

Score = 33.6 bits (75), Expect = 0.45
 Identities = 20/67 (29%), Positives = 32/67 (46%), Gaps = 12/67 (17%)

Query: 157 EWYVEIIVR-VEINGQ-----DLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204
 +W +E + + INGQ D + E +D+ IVD T + P+K+ E
 Sbjct: 14 QWTFESAVQENISINGQAWQEASDNCFMDSIKVLEDQFDEIIVDIATKRKQYPRKILEC 73

Query: 205 AVKSIKA 211
 +K+IKA
 Sbjct: 74 VIKTIKA 80

>STR:AAF86877|AAF86877|DC8. >GNP:AF201941|AF201941_1|Homo sapiens
 DC8 (DC8) mRNA, complete cds.
 Length = 268

Score = 33.6 bits (75), Expect = 0.45
 Identities = 20/67 (29%), Positives = 32/67 (46%), Gaps = 12/67 (17%)

Query: 157 EWYVEIIVR-VEINGQ-----DLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204
 +W +E + + INGQ D + E +D+ IVD T + P+K+ E
 Sbjct: 64 QWTFESAVQENISINGQAWQEASDNCFMDSIKVLEDQFDEIIVDIATKRKQYPRKILEC 123

Query: 205 AVKSIKA 211
 +K+IKA
 Sbjct: 124 VIKTIKA 130

>RTR:AAD53859|AAD53859|IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 (FRAGMENT). >GNP:AF174113|AF174113_1|Homo sapiens clone
 sc77u-36 immunoglobulin heavy chain variable region
 (IgH) mRNA, partial cds.
 Length = 122

Score = 31.7 bits (70), Expect = 1.7
 Identities = 27/101 (26%), Positives = 44/101 (42%), Gaps = 21/101 (20%)

Query: 143 SLYTGSWYTPIRR-----EWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
 S+ +GS +++ IR+ EW I R+ +G NY+ S+ T ++
 Sbjct: 28 SISSGSYYWSWIRQPAGKGLEW-----IGRIYTSGST-----NYNPSLKSRTVISVD 74

Query: 197 LPKKVFEAAVKSIIKAASSTEKF--PDGFWLGEQLVCWQAGT 235
 K F + S+ AA + + DG W GE + W GT

Sbjct: 75 TSKNQFSLKLSSVTAADTAVYYCARDGLWFGFISHWGQGT 115

>SP:Q99712 Q99446 O00564|IRKF_HUMAN|ATP-SENSITIVE INWARD RECTIFIER
 POTASSIUM CHANNEL 15 (POTASSIUMCHANNEL, INWARDLY
 RECTIFYING, SUBFAMILY J, MEMBER 15) (INWARDRECTIFIER
 POTASSIUM CHANNEL KIR 4.2) (KIR1.3).
 >GSP:W26369|W26369|Human kidney inward rectifier K
 channel 3 (KIRK-3). >GNP:U73191|U73191_1|Human inward
 rectifier potassium channel (Kir1.3), complete cds.
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSLYTGSLWYTPIRREWYYEVII 164
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

>GNP:D87291|D87291_1|Human mRNA for inward rectifier potassium
 channel, complete cds; human homolog of rat inward
 rectifier potassium channel 10.
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSLYTGSLWYTPIRREWYYEVII 164
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

>GNP:Y10745|Y10745_1|H.sapiens mRNA for inwardly rectifying potassium
 channel Kir4.2.
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSLYTGSLWYTPIRREWYYEVII 164
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens

Posted date: Oct 5, 2000 10:09 AM

Number of letters in database: 24,820,038

Number of sequences in database: 113,759

Lambda	K	H
0.321	0.138	0.435

Gapped		
Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 18424685

Number of Sequences: 113759

Number of extensions: 771118

Number of successful extensions: 1268

Number of sequences better than 10.0: 50

Number of HSP's better than 10.0 without gapping: 45

Number of HSP's successfully gapped in prelim test: 5

Number of HSP's that attempted gapping in prelim test: 1184

Number of HSP's gapped (non-prelim): 60

length of query: 351

length of database: 24,820,038

effective HSP length: 47

effective length of query: 304

effective length of database: 19473365

effective search space: 5919902960

effective search space used: 5919902960

T: 11